Figure 1:

Comparison of the predicted amino acid sequence of the *T. aureum* probe 'TA-PKS-1-consensus' and the homologous region on ORF A of *Schizochytrium* PKS gene cluster (Accession number AAK72879).

```
Quality:    1269              Length:    525
Ratio:  2.469                 Gaps:      10
Percent Similarity: 61.690    Percent Identity: 52.849

         Match display thresholds for the alignment(s):
                    | = IDENTITY
                    : = 2
                    . = 1


 TA-PKS-1-consensus.pep x aak72879.genpept..



    1 LCKTLDLEWPH..VFARSIDIELGANEETAAQAIFEELSCPDLTVREAGY 48
      ||||: |||     ||.| :||  |  . | || || |:.| |: :|| |
 2277 LCKTIGLEWSESDVFSRGVDIAQGMHPEDAAVAIVREMACADIRIREVGI 2326

   49 TKDGKRWTTEARPVGLGKPKQALRSSDVFLVSGGARGITPVCVRELAKSI 98
      . .| |  |  .  | |.. :   || ||||||||||.|:||: : |
 2327 GANQQRCTIRAAKLETGNPQRQIAKDDVLLVSGGARGITPLCIREITRQI 2376

   99 SGGTFVLLGRSPL.ADDPAWACGV.EEANIGTAAMAHLKAEFAAGRGPKP 146
      .|| ::|||||  . | :||| |: :|  :  ||  || |.|| ||||
 2377 AGGKYILLGRSKVSASEPAWCAGITDEKAVQKAATQELKRAFSAGEGPKP 2426

  147 TPKAHKALVGSVLGAREVLGSLESIRAQGARAEYVSCDVSCAERVKAVVD 196
      ||:|   |||||||||||| |: .| | | :| | ||||. | |    |
 2427 TPRAVTKLVGSVLGAREVRSSIAAIEALGGKAIYSSCDVNSAADVAKAVR 2476

  197 DLERRVGA.VTGVVHASGVLRDKSVERLELADFEVVYGTKVDGLLNLLQA 245
      | |  ..|| |.|:||||||||: :|:     :|: |:|||| || ||| |
 2477 DAESQLGARVSGIVHASGVLRDRLIEKKLPDEFDAVFGTKVTGLENLLAA 2526

  246 VDRPKLRHLVLFSSLAGFHGNTGQAVYAMANEALNKMAFHLETAMPGLSV 295
      |||   |:|:||||||||||||||||||.||. |||||||||||  || |  .||
 2527 VDRANLKHMVLFSSLAGFHGNVGQSDYAMANEALNKMG..LELA.KDVSV 2573

  296 KTIGFGPWDGGMVNDALKAHFASMGVQIIPLDGGAETVSRIIGACSPTQV 345
      |.| |||||||||   || |  |||||| :|||:||.|.|:   || ::
 2574 KSICFGPWDGGMVTPQLKKQFQEMGVQIIPREGGADTVARIVLGSSPAEI 2623

  346 LVGNWGLPPVVPNASVHKITVRLGGESANPFLSSHTIQGRKVLPMTXALG 395
      |||||  |      .  :  ::  .| ||||  | ||||:|||||  |:|
 2624 LVGNWRTPSKKVGSDTITLHRKISAKS.NPFLEDHVIQGRRVLPMTLAIG 2672
```

```
 396 LLAEAARGLYVGHQVXGIEDAQVFQGVVLDKGATCEVQLRRESSTASPSE 445
     |||   ||: |: .  |:|||.|.|| .|    ||| |    |||
2673 SLAETCLGLFPGYSLWAIDDAQLFKGVTVDGDVNCEVTL..TPSTAPSGR 2720

 446 VVLSASLNVFAAGKVVPAYRAHVVLGASGPRTGGVQLELKDLGVDADPAC 495
     | . |.|  |..||.||||| :||   |       ::   |  |||||
2721 VNVQATLKTFSSGKLVPAYRAVIVLSNQGAPPANATMQPPSL..DADPAL 2768

 496 SVGKGALYDGRTLFHGPAFQYMDEV 520
      .|..|||:|||||||. .|:|
2769 ...QGSVYDGKTLFHGPAFRGIDDV 2790
```

Figure 2:

Comparison of the predicted amino acid sequence of the *T. aureum* probe 'TA-PKS-1-consensus' and the homologous region on ORF 5 of *Shewanella* PKS gene cluster (Accession number AAB81123).

```
Quality:      641        Length:      551
Ratio:    1.233          Gaps:        16
Percent Similarity: 47.379   Percent Identity: 39.919

           Match display thresholds for the alignment(s):
                      | = IDENTITY
                      : = 2
                      . = 1


  TA-PKS-1-consensus.pep  x  aab81123.genpept


     1 LCKTLDLEWPHVFARSIDIELGANEETAAQAIFEELSCPDLTVREAGYTK 50
       | ||| ||| || |.:||     .    | || ||     . | | .
  2094 LTKTLSHEWPQVFCRALDIATDVDATHLADAITSELFDSQAQLPEVGLSL 2143

    51 .DGK..RWTTEARPVGLGKPKQALRSSDVFLVSGGARGITPVCVRELAKS 97
       |||   | |    |         | | |.| ||.|||:|:|  |   || |
  2144 IDGKVNRVTLVAAEAADKTAKAELNSTDKILVTGGAKGVTFECALALA.S 2192

    98 ISGGTFVLLGRSPLADDPAWACGVEEANIGTAAMAHLKAEFAAGRGPKPT 147
       |    |:| ||| |    |.|| | :  : .||.||:        | |||
  2193 RSQSHFILAGRSELQALPSWAEGKQTSELKSAAIAHI.....ISTGQKPT 2237

   148 PKAHKALVGSVLGAREVLGSLESIRAQGARAEYVSCDVSCAERVKAVVDD 197
       || .| | |  .|:  .| .    || |||||| ||.   : |
  2238 PKQVEAAVWPVQSSIEINAALAAFNKVGASAEYVSMDVTDSAAITAA... 2284

   198 LERRVGAVTGVVHASGVLRDKSVERLELADFEVVYGTKVDGLLNLLQAVD 247
       |   |  :||.:| .||| || ::   ||:   ||||||.|| || |.:
  2285 LNGRSNEITGLIHGAGVLADKHIQDKTLAELAKVYGTKVNGLKALLAALE 2334

   248 RPKLRHLVLFSSLAGFHGNTGQAVYAMANEALNKMAFHLETAMPGLSVKT 297
       |:: | :||| |||:|| ||. |||.|: ||| |      |   | .
  2335 PSKIKLLAMFSSAAGFYGNIGQSDYAMSNDILNKAALQFTARNPQAKVMS 2384

   298 IGFGPWDGGMVNDALKAHFASMGVQIIPLDGGAETVSRIIGACSPTQVLV 347
       .||||||||| |||   |  :|||  |||  . : | .  |.|:
  2385 FNWGPWDGGMVNPALKKMFTERGVYVIPLKAGAELFATQLLAETGVQLLI 2434

   348 G....................NWG..LPPVVPNASVHK......IT.VRLG 369
       |                    | |  | |  | |    :| ||
  2435 GTSMQGGSDTKATETASVKKLNAGEVLSASHPRAGAQKTPLQAVTATRLL 2484

   370 GESANPFLSSHTIQGRKVLPMTXALGLLAEAARGLYVGHQVXGIEDAQVF 419
       || |: | | | ||| |:  : ||| : .| ||  : |  ..
```

```
2485 TPSAMVFIEDHRIGGNSVLPTVCAIDWMREAASDM.LGAQVK.VLDYKLL 2532
          .        .        .        .        .
 420 QGVVLDKGATCEVQLRRESSTASPSEVVLSASLNVFAAGKVVPAYRAHVV 469
     .|:|  :      |. | |  .     | | | :.    |:  | |:| .:
2533 KGIVFETDEPQELTL..ELTPDDSDEATLQALIS..CNGR..PQYKATLI 2576
          .        .        .        .        .
 470 LGASGPRTGGVQLELKDLGVDADPACSVGKGALYDGRTLFHGPAFQYMDE 519
       .  :     | :|     .  | . |  || |||||| | .
2577 SDNADIKQLNKQFDL......SAKAITTAK.ELYSNGTLFHGPRLQGIQS 2619

 520 V 520
     |
2620 V 2620
```
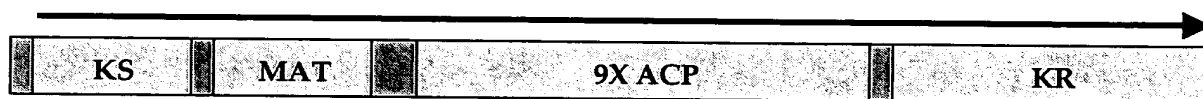
Figure 3:

Organization of PUFA-PKS genes from *Thraustochytrium aureum* ATCC 34304

ORF A- 8748 bp

ORF B- 6123 bp

KS= β-keto acyl synthase

MAT= MalonylCoA

transferase

ACP= Acyl carrier protein

KR= Ketoacyl-ACP reductase

AT= Acyl transferase

FIGURE 4

Sequence ID Nos. and Corresponding Sequences:

SEQ ID NO 1:

5'-AGC GGA TAA CAA TTT CAC ACA GG-3'

SEQ ID NO 2:

CACGAGGCCAAGCATTCGAGCAAAGCGCTCAACCAGCAGATCCCAGG

CGGGCGCGCCTGCTTCGTGGGCGTCTCGCGAATCGACGGACAGCTCG

GACTTAGCGGAGCTTGCGCGAAAGGAAAGGGCTGGGCTGAGGCCGCA

GAGATTGCTCAGCAAGGAGCCGTCGCAGGCTTGTGCAAGACCTTGGA

CCTAGAGTGGCCGCACGTCTTCGCTCGCAGCATCGACATCGAGCTTGG

CGCGAACGAAGAAACAGCTGCGCAAGCAATCTTTGAGGAGCTCTCTT

GCCCGGACCTAACGGTGCGCGAAGCAGGATACACCAAAGACGGCAA

GCGGTGGACGACTGAGGCGCGACCGGTTGGGCTTGGCAAGCCCAAGC

AGGCACTACGTTCTTCGGACGTCTTCTTGGTTTCTGGTGGGGCGCGGGG

AATTACACCTGTTTGCGTTCGCGAGTTGGCCAAATCGATCAGTGGTGG

CACTTTTGTCCTCCTCGGGCGGTCCCCTCTCGCTGATGATCCGGCGTGG

GCTTGCGGCGTCGAGGAAGCAAACATTGGGACAGCCGCTATGGCGCA

CCTCAAGGCCGAGTTCGCAGCCGGGCGCGGCCCGAAGCCGACGCCAA

AGGCCCACAAAGCACTCGTTGGGAGCGTCCTGGGGGCGCGCGAAGTC

CTTGGTTCGCTAGAGAGTATTCGCGCCCAGGGTGCGCGCGCCGAGTAC

GT

SEQ ID NO:3:

TCGCCAACACAAGTTCTGGTTGGCAACTGGGGCTTGCCCCCTGTAGTT

CCTAACGCGAGCGTGCACAAGATTACTGTGAGGCTTGGCGGGGAGTC

TGCAAACCCTTTCCTGTCCTCCCACACGATTCAAGGCAGAAAGGTCTT

GCCGATGACTGYGGCGCTTGGGCTTCTCGCTGAGGCGGCTCGAGGGCT

CTACGTCGGTCACCAAGTAGYCGGGATTGAGGACGCCCAAGTCTTCCA

GGGAGTCGTGTTGGACAAAGGGGCGACGTGTGAGGTCCAGCTTCGCC

GCGAGTCTTCGACTGCAAGCCCAAGCGAGGTTGTGCTGAGTGCTTCGC

TCAATGTATTCGCGGCGGGAAAGGTTGTGCCTGCGTACCGCGCGCATG

TCGTGCTCGGCGCTTCAGGGCCACGCACTGGCGGCGTGCAGCTTGAAC

TGAAAGATTTGGGCGTGGACGCCGACCCTGCTTGCTCCGTTGGCAAGG

GTGCGCTGTACGACGGTAGGACGCTGTTCCATGGGCCGGCGTTTCAGT

ACATGGATGAGGTTCCCTGGTGCTCGCCTGCAGAGCTTGCCGTGCGGT

GCCGTGTCGTTCCGAGCGCGGCTCAGGACCGCGGCCAATATGTTTCGC

GCGGAGTGTTGTACGACCCGTTCCTGAACGACACGGTGTTTCAAGCTC

TCCTTGTTTGGGCCCGTCTGGTCAGGGACAGCGCTTCGCTACCGAGCA

ACGTTGAACGAATCTCGTTCCACGGCCAGCCGCCGAGCGAGGGCGAG

GTGTAGTACACCACGCTCAAGCTGGACAGTGCTGCGAGCGGGCCGCT

CGACCCGATTGCAACAGGCGCATTTCTTCCTCCACCGAGCTTGCGGGG

CGGTCTTTGCATCAGGGCGAGCGAGTGTGGTTCTGAACAAGGCTCTTT

CGTATGATGGCTCTCGACCCAAAGGCGAGTAGAGTACTCTACTCAGTA

CTCCTTTTCACATACCGGCAGGCAGCGTTGCTGTGGGATGGCCGGGGG

CTCTTCTGCACGCGGCTCC

SEQ ID NO: 4:

GAATTCGGCACGAGGCCGGCCTCACGACGCAGGTTGTTCGGTTCCGCG

CTGCAGGTCTGTCACGCAACGCGGACGGCTCTGTTCGAGTCCGCAACC

GCATCATCGGAAAGATTTCGCGCACGGAGCTCGCGGAGATGTTCATTC

GCCCCGCTCCGGAGGCCCTCTTGACCAAGTTGGTTGCGTCGGGTGAGA

TTTCGGCCGAGCAGMNGCCTGGCCAAACAAGTGCCGATGCCGACGAC

ATTGCCGTCGAGSAGAACTCGGGCGGCCACACGGACAATCGCCCGAT

CCATGTCATCCTTCCGCTGATCATCGCGCTCCGCAACAGGCTGCACAA

GGAGTGCGGTTACCCGGCGAGCCTTCGCGTTCGAGTTGGCGCGGGTGG

CGGGATCGGCTGCCCGCTTGCAGCAACTGCGGCCTTCAACATGGGCGC
CGCCTTTCTCGTGACAGGAACAGTCAACCAACTCAGCCGGCAGTCGG
GCACCTGCGACGCGGTGCGCATSAGCTTTTCAAAAGCGACCTACTCGG
ACATCACAATGGCGCCCGCCGCAGATATGTTTGACCAGGGGGTTGAG
CTCCAGGTGCTCAAGAAGGGCACCATGTTTCCGTCGCGCGCCAAGAA
GCTCTACGAGCTGTTTTGCACGTACAACTCGKTCGACGAGATGCCCGC
CGAGGAGCTCGCGCGGGTTGAGAAGCSGATYTTCCAAAAGCCCCTCG
CGGSCGTATGGGACGAGACGAAAGACTTTTACATCAACCGTCTCCACA
ACGAGGACAAGATCGAACGCGCAGAAAGGATGGCAAGCTCAAGAT
GTCGCTCTCGTTCCGCTGGTACCTTGGCCTGAGTTCGTTCTGGGCCAAC
AATGGAATCGCCGACCGCGTGCTGGACTATCAAGTGTGGTGCGGCCCT
GCGATTGGGGCCTGGAACGACTTTGCCAAGGGATCCTACCTCGACGCC
GAGGTCTGCGGCCAGTTTCCTTGCGTTGTGCAGGTCAACCTGCAGATC
CTCCACGCGCGGCCTACATGCAGCGCCTTCTGGCCGTCAAGCATGACC
CGCGCATCGAGTTTGACCTCGAGGACCCGGTCTTTGGTACGCCCCCAC
TGCCGCGCTCTAAAGCGATGCAGCAACGCACTCTTTCGGAGGCCCGTC
GCTGCAGCACTTGTGCGAACTCGATAGGGTTTCTTTCAAGATTTCAATC
AACAAAACAAGTATTGGAATGACAAAAAAAAAAAAAAAAAACTCGAG

SEQ ID NO:5:

5'- CTT GTG CAA GAC CTT GGA CCT AGA G-3'

SEQ ID NO:6:

5'-GAA CCT CAT CCA TGT ACT GAA ACG C-3'

SEQ ID NO:7:

TTGTGCAAGA CCTTGGACCT AGAGTGGCCG CACGTCTTCG

CTCGCAGCATCGACATCGAG CTTGGCGCGA ACGAAGAAAC

AGCTGCGCAA GCAATCTTTGAGGAGCTCTC TTGCCCGGAC

CTAACGGTGC GCGAAGCAGG ATACACCAAAGACGGCAAGC

GGTGGACGAC TGAGGCGCGA CCGGTTGGGC TTGGCAAGCC

CAAGCAGGCA CTACGTTCTT CGGACGTCTT CTTGGTTTCT

GGTGGGGCGCGGGGAATTAC ACCTGTTTGC GTTCGCGAGT

TGGCCAAATC GATCAGTGGTGGCACTTTTG TCCTCCTCGG

 GCGGTCCCCT CTCGCTGATG ATCCGGCGTGGGCTTGCGGC

GTCGAGGAAG CAAACATTGG GACAGCCGCT ATGGCGCACC

TCAAGGCCGA GTTCGCAGCC GGGCGCGGCC CGAAGCCGAC

GCCAAAGGCCCACAAAGCAC TCGTTGGGAG CGTCCTGGGG

GCGCGCGAAG TCCTTGGTTCGCTAGAGAGT ATTCGCGCCC

AGGGTGCGCG CGCCGAGTAC GTTTCCTGCGACGTTTCGTG

TGCGGAGCGC GTCAAGGCCG TCGTCGACGA TCTCGAGCGA

CGGGTCGGGG CTGTAACTGG GGTTGTGCAC GCCTCTGGTG

TTCTCCGAGACAAGTCCGTT GAGCGCTTGG AGCTCGCCGA

CTTCGAGGTC GTGTACGGCACCAAGGTGGA CGGCCTGCTC

AACCTGCTGC AGGCCGTGGA CCGCCCCAAACTCCGGCACT

TGGTCCTCTT CAGCTCCCTG GCCGGTTTCC ACGGCAACAC

TGGGCAGGCC GTGTACGCTA TGGCGAATGA GGCGCTGAAC

AAGATGGCCTTCCATTTGGA AACTGCGATG CCTGGCCTCT

CGGTCAAGAC GATCGGGTTTGGACCTTGGG ACGGCGGCAT

GGTCAACGAT GCGCTGAAAG CGCACTTTGCGTCTATGGGC

GTCCAAATTA TTCCGCTCGA CGGYGGCGCG GAGACCGTTT

CCCGAATCAT CGGGGCGTGC TCGCCAACAC AAGTTCTGGT

TGGCAACTGGGGCTTGCCCC CTGTAGTTCC TAACGCGAGC

GTGCACAAGA TTACTGTGAGGCTTGGCGGG GAGTCTGCAA

ACCCTTTCCT GTCCTCCCAC ACGATTCAAGGCAGAAAGGT

CTTGCCGATG ACTGYGGCGC TTGGGCTTCT CGCTGAGGCG

GCTCGAGGGC TCTACGTCGG TCACCAAGTA GYCGGGATTG

AGGACGCCCAAGTCTTCCAG GGAGTCGTGT TGGACAAAGG

GGCGACGTGT GAGGTCCAGCTTCGCCGCGA GTCTTCGACT

GCAAGCCCAA GCGAGGTTGT GCTGAGTGCTTCGCTCAATG

TATTCGCGGC GGGAAAGGTT GTGCCTGCGT ACCGCGCGCA

TGTCGTGCTC GGCGCTTCAG GGCCACGCAC TGGCGGCGTG

CAGCTTGAACTGAAAGATTT GGGCGTGGAC GCCGACCCTG

CTTGCTCCGT TGGCAAGGGTGCGCTGTACG ACGGTAGGAC

GCTGTTCCAT GGGCCGGCGT TTCAGTACATGGATGAGGTT C

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AGAGCACCGCCGAGACCAAGAGCCGAGGCAGACAAGGCCAGCAACG

AGATGGAGACAAAGGACGATCGCGTTGCGATCGTGGGCATGTCGGCC

ATACTGCCTTGCGGTGAGTCAGTGCGCGAGTCGTGGGAGGCGATTCGC

GAGGGGCTCGATTGCCTGCAGGACCTGCCTGCGGACCGAGTCGATAT

CACGGCGTACTACGACCCGAACAAGACAACCAAGGACAAGATCTACT

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GCCTCGACTCGTTCCCTGGGTTTCTTGGCAACGTGACCGCCGGGCGGT

GCAGCAACGTCTTCAACATGGAAGGCATGAACTGCGTCGTGGACGCT

GCGTGCGCCAGCTCGCTCATCGCGATCAAGGTTGCCATTGATGAGCTC

CTCCACGGGGACTGCGACACCATGATTGCCGGTGCGACCTGCACCGA

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CGCATGAACCAAGTTCCACAACCGGTGCTCTTGCACGCAAGCTCCGCG

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GCCGTCTCGCCCGAAGCCAGCAAGCACGCAGACTACCGCGCCATCGT

AGCGTTCCATGAAGCGTTTAAGCTTCGCGCTGGAGTGCCGGCCGGCCA

TGCTCGAATTGGCTTTGTGTCCGGCAGCGCGGCAGCAACGCTTGCAGT

GCTCCGAGCCGCCTCTGCAAAACTCAAGCAGTCGAGTGCGACGCTCG

AATGGACCCTGCTCCGCGAGGGCGTCACGTACCGCTCCGCCGCGATG

CACACTCCTGGCAGTGTCGCTGCTCTGTTTGCCGGGCAAGGCGCGCAG

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GCTGGTCTTGCGCCCGACCACGTCGCGGGTCATTCTCTCGGCGAGTTT

GGTGCTTTGCTCGCCGCTGGATGCGCAAGCCGTGAGGAGCTCTTCCGT

CTGGTCTGCAGCAGAGCGAAGGCAATGCAAGACGTTCCCAAGCCAAG

CGAGGGCGTCATGGCAGCTGTCATCGGCCGTGGTGCTGACAAGCTCA

CGCTGCAAGGCGATGGTGCGTGGCTTGCCAACTGCAACTCGCCAAGC

CAAGTGGTCATTTCCGGCGACAAGACTGCTGTCGAGCGTGAATCCAGC

CGGTTGGCAGGCCTTGGCTTCAGGATCATTCCGCTTGCATGCGAAGGC

GCCTTCCATTCACCGCACATGACGGCGGCCCAGGCCACGTTTCAGGCT

GCACTGGACAGCCTCAAGATCTCCACCCCGACGAACGGGGCGCGCCT

GTACAACAACGTTTCCGGAAAGACCTGCCGATCCCTGGGTGAACTCC

GCGACTGCCTGGGCAAGCACATGACAAGTCCTGTGCTCTTCCAGGCAC

AGGTAGAGAACATGTACGCTGCCGGGGCGCGCATTTTCGTGGAGTTTG

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AGGACGTCGACGCGCTCAGCCGCACACGAACAGTTGGCGAGGTCGTT

GACGCCATGAAGGCTGAGATCGGCGGGCAAGCGACCAGTGCGCCTTC

GCCGATGGCCCAGCCCCAAGCCTCAGCACCATCACCGTCCCCTACTGC

CTCTGTGCTGCCTAAGCCTGTTGCTTACCAGCTAGTGTCGATCCCGCC

AAGCTCGCGCGCGCCGAAGCGGTCGTCATGGAGGTTCTCGCCGCCAA

GACTGGCTACGAGGTCGACATGATCGAGGCTGACATGCTGCTCGACG

CCGAGCTCGGCATCGACTCGGTCAAGCGCATTGAGATCCTGGCGGCTG

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CCTCAGCACCATCACCGTCCGCAACAACTGCCTCTGTGCTGCCTAAGC

CTGTTGCTGCACCAACTAGCGCCGATCCCGCCAAGCTCGCGCGCGCCG

AAGCCGTCGTCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCG

ACATGATCGAGGCTGACATGCTGCTCGACGCCGAGCTCGGCATCGACT

CGGTCAAGCGCATTGAGATCCTGGCGGCTGTCCAAGCCCAGCTCGGG

GTCGAGGCCAAGGACGTCGACGCGCTCAGCCGCACACGCACGGTTGG

CGAGGTCGTCGAGGCCATGAAGGCTGAGATCGGCGGGCAAGCGACC

AGTGCACCTGCGTCCGTGGCCCAGCCCCAAATCTCTGTGTCCCCTACG

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GAAGCCGTCGTCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTC

GACATGATCGAGGCTGACATGCTGCTCGACGCCGAGCTCGGCATCGA

CTCCGTCAAGCGCATCGAGATCCTGGCGGCTGTCCAGGCCCAGCTCGG

GGTCGAGGCCAAGGACGTCGACGCGCTCAGCCGCACACGCACTGTTG

GCGAGGTCGTTGACGCCATGAAGGCTGAGATCGGCGGGCAAGCGACC

AGTGCGCCTGCATCCGTGGCCCAGCCCCAAGCCTCAGCACCGTCGCC

GTCCGCTACTGCCTCTGTGCTGCCTAAGCCTGTTGCTGCACCAACTAGC

GCCGATCCCGCCAAGCTCGCGCGCGCCGAAGCCGTCGTCATGGAGGT

TCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCGAGGCTGACAT

GCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAAGCGCATCGAGA

TCCTGGCGGCTGTCCAAGCCCAGCTCGGGGTCGAGGCCAAGGACGTC

GACGCGCTCAGCCGCACACGCACGGTTGGCGAGGTCGTCGAGGCCAT

GAAGGCTGAGATCGGCGGGCAAGCGACCAGTGCACCTGCGTCCATGG

CCCAGCCCCAAATCTCTGTGTCCCCTACGCCTCTCGCTGCATCTCCTAG

TGCCGATCCTGCCAAGCTCGCGCGCGCCGAGGCCGTCGTCATGGAGGT

TCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCGAGGCCGACA

TGCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAAGCGCATCGAG

ATCCTGGCGGCTGTCCAAGCTCAGCTCGGGGTCGAGGCCAAGGACGT

CGACGCGCTCAGCCGCACACGCACGGTTGGCGAGGTCGTTGATGCCA

TGAAGGCTGAGATCGGCGGGCAAGCGACCAGTGCGCCTGCATCCGTG

GCCCAGCCCCAAGCCTCAGCACCGTCGCCGTCCGCTACTGCCTCTGCG

CCTGTTACGCCTCTCGCTGCACCAGCTAGTGTCGATCCCGCCAAGCTC

GCGCGCGCCGAAGCCGTCGTCATGGAGGTTCTCGCCGCCAAGACTGG

CTACGAGGTCGACATGATCGAGGCTGACATGCTGCTCGACGCCGAGC

TCGGCATCGACTCCGTCAAGCGGATTGAGATCCTGGCGGCTGTCCAAG

CCCAGCTCGGGGTCGAGGCCAAGGACGTCGACGCGCTCAGCCGCACA

CGCACTGTTGGCGAGGTCGTTGACGCCATGAAGGCTGAGATCGGCGG

GCAAGCGACCAGCGCACCTGCGTCCGTGGCCCAGCCCCAAGCCTCAG

CACCGTCGCCGTCCGCTACTGCCTCTGTGCTGCCTAAGCCTGTTGCTTC

ACCAGCTAGTGTCGATCCCGCCAAGCTCGCGCGCGCCGAAGCGGTCG

TCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCG

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CGCATGAACCAAGTTCCACAACCGGTGCTCTTGCACGCAAGCTCCGCG

TCAGCTCTT

SEQ ID NO:13:

METKDDRVAIVGMSAILPCGESVRESWEAIREGLDCLQDLPADRVDITAYY

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FTK

KKKNIGCVLGIGGGQKASHEFYSRLNYVVVEKVLRKMNLPDEVVEAAVEK

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KGRKETVAVG SIKSQIGHLK

AVAGFAGLVKVVMALKHKTLPQTINVHDPP

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SEQ ID NO:14:

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SEQ ID NO:15:

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NWPPFRSAVQEMDAAQVTAAAPKRLSEVLYPRKPYAAEPEQDNKAISMTI

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FRLVCSRAKAMQDVPKPSEGVMAAVIGRGADKLTLQGDGAWLANCNSP

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YAAGARIFVEFGPKQVLSKLVGEILADKSDFVTVAVNSSSSKDSDVQLREA

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SEQ ID NO:16:

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GAGGCCGACATGCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAA

GCGCATTGAGATCCTGGCAGCTGTCCAGGCCCAGCTCGGGGTCGAGG

CCAAGGACGTCGACGCGCTCAGCCGCACACGAACAGTTGGCGAGGTC

GTTGACGCCATGAAGGCTGAGATCGGCGGG

SEQ ID NO:17:

QVTSAPIAELARAEAVVMEVLAAKTGYEVDMIEADMLLDAELGIDSVKRIE

ILAAVQAQLGVEAKDVDAL SRTRTVGEVVDAMKAEIGG

SEQ ID NO:18:

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TGGTTGAGATTGCTCGTTGCAGCGAACTAGCTCTGGAGCGCCCGATGG

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AGCTAGGGACCAGCTTGGCTTTGCCCTGCTGCTTGCCAAGCATTCGAG

CAAAGCGCTCAACCAGCAGATCCCAGGCGGGCGCGCCTGCTTCGTGG

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AAAGGAAAGGGCTGGGCTGAGGCCGCAGAGATTGCTCAGCAAGGAG

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GACCGGTTGGGCTTGGCAAGCCCAAGCAGGCACTACGTTCTTCGGAC

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GCGAGTTGGCCAAATCGATCAGTGGTGGCACTTTTGTCCTCCTCGGGC

GGTCCCCTCTCGCTGATGATCCGGCGTGGGCTTGCGGCGTCGAGGAAG

CAAACATTGGGACAGCCGCTATGGCGCACCTCAAGGCCGAGTTCGCA

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TTCGCGCCCAGGGTGCGCGCGCCGAGTACGTTTCCTGCGACGTTTCGT

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GGGGCTGTAACTGGGGTTGTGCACGCCTCTGGTGTTCTCCGAGACAAG

TCCGTTGAGCGCTTGGAGCTCGCCGACTTCGAGGTCGTGTACGGCACC

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E

10   YVSCDVSCAERVKAVVDDLERRVGAVTGVVHASGVLRDKSVERLELADFE

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NKMAFHLETAMPGLSVKTIGFGPWDGGMVNDALKAHFASMGVQIIPLDG

G

15   AETVSRIIGACSPTQVLVGNWGLPPVVPNASVHKITVRLGGESANPFLSS

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T

CEVQLRRESSTASPSEVVLSASLNVFAAGKVVPAYRAHVVLGASGPRTGG

VQLELKDLGVDADPACSVGKGALYDGRTLFHGPAFQYMDEVLRCSPAEL

20   A

VRCRVVPSAAQDRGQFVSRGVLYDPFLNDTVFQALLVWARLVRDSASLPS

NVERISFHGQPPSEGEVFYTTLKLDSAASGPLDPIAKAQFFLHRACGAVF

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TCCTTGCAATGGAGCGCGGCGTGATCCCCCCGACCCCGGGCGTTGACTCT

GGCACCCAGATTGATCCCCTCGTCGTCACAGCGGCGCTCCCGTGGCCGGA

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SEQ ID NO: 21:

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GGAAGGGGCCAACTCGGTCCATCGGTGCGCCCAGCTCGCCAAGTACATG

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CGGGAGCGCCGAGGCGTTCTTCGTGAGGTCGCGCCGCATGCAGATCTCGA
AAAGTCAGCGCCCGGCCGCGCCGTTTGACCGCGCCGCAGACGGCTTCTTC
GCGGGGGAAGGGTGCGGCGCCCTCGTCTTCAAACGCCTGACTGACTGTGT
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CGCCGCGCCGCTCTTCGTGCTGCCGCAGGGTCGGCGCGGGTTGACCCA
GCCAGCATCGACATGGTCGAGCTGAGCGCAGATTCCCACCGGTTTGTGCG
GGCGCCAGGCACCGTGGCTCAGCCTCTGACAGCCGAAGTCGAGGTCGGG
GCGGTGCGGGAAGTGATCGGGACCGCGGGGAGGGGCTCTCGAAGCGTGG
CCGTCGGATCGGTCCGCGCCAACGTCGGGGACGCAGGGTTTGCTTCCGGG
GCCGCTGCCCTCGTAAAAACTGCGCTCTGCTTGCACAACCGCTACTTGGC
GGCTACCCCAGGCTGGGATGCGCCTGCTGCCGGCGTGGATTTTGGTGCCG
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GCACGGCACGCCGCAATTTCTGGCGTGGACGAAGGCGGGTCG

SEQ ID NO:23:

QPRLGSGPNRKLAIVGMDATFGSLKGLSALEAALYEARHAARPLPAKRWRFL
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AILDSGLAKGGNVAVLVGLGTDLELYRHRARVALKERLQGLVRSAEGGALTS
RLMNYINDSGTSTSYTSYIGNLVATRVSSQWGFTGPSFTVTEGANSVHRCAQL
AKYMLDRGEVDAVVVAGVDLCGSAEAFFVRSRRMQISKSQRPAAPFDRAAD
GFFAGEGCGALVFKRLTDCVSGERIYASLDSVVVATTPRAALRAAAGSARVDP
ASIDMVELSADSHRFVRAPGTVAQPLTAEVEVGAVREVIGTAGRGSRSVAVGS
VRANVGDAGFASGAAALVKTALCLHNRYLAATPGWDAPAAGVDFGAELYV
CRESRAWVKNAGVARHAAISGVDEGGS

SEQ ID NO:24:

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GAGCAAGCCGACGGCTTGAGCGCCGCCGCGGCTGCCGTAGACCGCTTAC

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AVEFNALRKLWGVAPGAPVDSFWQGYVVRATRAQVEQAIGEDNQFVRLLIV

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MLRFPSQDETGGCKMYSSVSNSRIGPVEESQMGPGTELVFSPSMEDFVAQLYSR

VADFPAITEAVYQQGHDVFVEVGPDHSRSAAVRSTLGPTRRHIAVAMDRKGE

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GCAAATTGGCCAGGACGCTTGCCATCGATGCTTGCGACTCCGACGTGCGC

GCCGCCTTGCTGGACCTGGACGCGCCAATCGCGGTCGGCGGCTCCTCGCG

CGCCCAAGTCCCGCCGTGCCCAGTGAGCGCGCTCGGAAGCGCCGCCTTTC

GAGCGGCACACGGCGTCGATTATGCGCTCTACATGGGCGCAATGGCCAA

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GGGAAAGCGCGGACGCGTTGGCGTACACGGTTGCGGAAGCCAGATAG

SEQ ID NO:27:

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ALYMGAMAKGVASAEMVIAAGKARMLASFGAGGLPLGEVEEALDKIQAALP

EGPFAVNLIHSPFDPNLEEGNVELFLRRGIRLVEASAFMSVTPSLVRYRVAGLE

RGPGGTARVLNRVIGKVSRAELAEMFMRPPPAAIVSKLLAQGLVTEEQASLAE

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SKWASTGQVGRELDYQVWCGPTIGAFNEFVKGSSLDAEACGGRFPCVVRVN

QEILCGAAYEQRLARFMLLAGRESADALAYTVAEAR